

## SEQUENCE LISTING

### (1) GENERAL INFORMATION

#### (i) APPLICANT: Hammond, H. Kirk

Insel, Paul A.

Ping, Peipei

Post, Steven R.

Gao, Meihua

#### (ii) TITLE OF THE INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE

#### (iii) NUMBER OF SEQUENCES: 13

#### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER

(B) STREET: 755 PAGE MILL ROAD

(C) CITY: PALO ALTO

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 94304-1018

#### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

#### (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: UNKNOWN

(B) FILING DATE: HERewith

(C) CLASSIFICATION:

#### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/472,667

(B) FILING DATE: December 27, 1999

#### (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: POLIZZI, CATHERINE M.

(B) REGISTRATION NUMBER: 40,130

(C) REFERENCE/DOCKET NUMBER: 220002056723

#### (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-813-5600

(B) TELEFAX: 650-494-0792  
 (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...312  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TCA TGG TTT AGT GGC CTC CTG GTC CCT AAA GTG GAT GAA CGG AAA  
 48

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys  
 1 5 10 15

ACA GCC TGG GGT GAA CGC AAT GGG CAG AAG CGT TCG CGG CGC CGT GGC  
 96

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly  
 20 25 30

ACT CGG GCA GGT GGC TTC TGC ACG CCC CGC TAT ATG AGC TGC CTC CGG  
 144

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg  
 35 40 45

GAT GCA GAG CCA CCC AGC CCC ACC CCT GCG GGC CCC CCT CGG TGC CCC  
 192

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro  
 50 55 60

TGG CAG GAT GAC GCC TTC ATC CGG AGG GGC GGC CCA NGC AAG GGC AAG  
 240

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys  
 65 70 75 80

GAA CTG GGG CTG CGG GCA GTG GCC CTG GGC TTC GAA GAT ACC GAA GTG  
288

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val  
85 90 95

ACA ACG ACA CCG GCG GGA CCG CTG AA  
Thr Thr Thr Pro Ala Gly Pro Leu  
100

314

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys  
1 5 10 15  
Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly  
20 25 30  
Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg  
35 40 45  
Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro  
50 55 60  
Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys  
65 70 75 80  
Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val  
85 90 95  
Thr Thr Thr Pro Ala Gly Pro Leu  
100

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1812

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTT AAC GTG GTG CTG GGC ATC CTG GCG GCA GTG CAG GTC GGG GGC GCT  
48

Val Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val Gly Gly Ala  
1 5 10 15

TTC GCA GCA GAC CCG CGC AGC CCC TCT GCG GGC CTC TGG TGC CCT GTG  
96

Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val  
20 25 30

TTC TTT GTA TAC ATC GCA TAC ACG CTC CTC CCC ATC CGC ATG CGG GCT 144  
Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala  
35 40 45

GCC GTC CTC AGC GGC CTG GGC CTC TCC ACC TTG CAT TTG ATC TTG GCC 192  
Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala  
50 55 60

TGG CAA CTT AAC CGT GGT GAT GCC TTC CTC TGG AAG CAG CTC GGT GCC  
240  
Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala  
65 70 75 80

AAT GTG CTG CTG TTC CTC TGC ACC AAC GTC ATT AGC ATC TGC ACA CAC  
288  
Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His  
85 90 95

TAT CCA GCA GAG GTG TCT CAG CGC CAG GCC TTT CAG GAG ACC CGC AGT  
336  
Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser  
100 105 110

TAC ATC CAG GCC CGG CTC CAC CTG CAG CAT GAG AAT CGG CAG CAG GAG  
384  
Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu

115                      120                      125

CGG CTG CTG CTG TCG GTA TTG CCC CAG CAC GTT GCC ATG GAG ATG AAA  
432

Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys  
130                      135                      140

GAA GAC ATC AAC ACA AAA AAA GAA GAC ATG TTC CAC AAG ATC TAC ATA  
480

Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile  
145                      150                      155                      160

CAG AAG CAT GAC AAT GTC AGC ATC CTG TTT GCA GAC ATT GAG GGC TTC  
528

Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe  
165                      170                      175

ACC AGC CTG GCA TCC CAG TGC ACT GCG CAG GAG CTG GTC ATG ACC CTG  
576

Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu  
180                      185                      190

AAT GAG CTC TTT GCC CGG TTT GAC AAG CTG GCT GCG GAG AAT CAC TGC  
624

Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys  
195                      200                      205

CTG AGG ATC AAG ATC TTG GGG GAC TGT TAC TAC TGT GTG TCA GGG CTG  
672

Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu  
210                      215                      220

CCG GAG GCC CGG GCC GAC CAT GCC CAC TGC TGT GTG GAG ATG GGG GTA  
720

Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val  
225                      230                      235                      240

GAC ATG ATT GAG GCC ATC TCG CTG GTA CGT GAG GTG ACA GGT GTG AAT  
768

Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn  
245                      250                      255

GTG AAC ATG CGC GTG GGC ATC CAC AGC GGG CGC GTG CAC TGC GGC GTC  
816

Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val

260                      265                      270

CTT GGC TTG CGG AAA TGG CAG TTC GAT GTG TGG TCC AAT GAT GTG ACC  
864

Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr  
275                      280                      285

CTG GCC AAC CAC ATG GAA GCA GGA AGC CGG GCT GGC CGC ATC CAC ATC  
912

Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile  
290                      295                      300

ACT CGG GCA ACA CTG CAG TAC CTG AAC GGG GAC TAC GAA GTG GAG CCA  
960

Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro  
305                      310                      315                      320

GGC CGT GGT GGC AAG CGC AAC GCG TAC CTC AAG GAG CAG CAC ATT GAG  
1008

Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu  
325                      330                      335

ACT TTC CTC ATC CTG GGC GCC AGC CAG AAA CGG AAA GAG GAG AAA GGC  
1056

Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly  
340                      345                      350

ATG CTG GCC AAG CTG CAG CGG ACT CGG GCC AAC TCC ATG GAA GGG CTG  
1104

Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu  
355                      360                      365

ATG CCG CGA TGG GTT CCT GAT CGT GCC TTC TCC CGG ACC AAG GAC TCC  
1152

Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser  
370                      375                      380

AAG GCC TTC CGC CAG ATG GGC ATT GAT GAT TCC AGC AAA GAC AAC CGG  
1200

Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg  
385                      390                      395                      400

GGC ACC CAA GAT GCC CTG AAC CCT GAG GAT GAG GTG GAT GAG TTC CTG  
1248

Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu

405                      410                      415

AGC CGT GCC ATC GAT GCC CGC AGC ATT GAT CAG CTG CGG AAG GAC CAT  
1296

Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His  
420                      425                      430

GTG CGC CGG TTT TTG CTC ACC TTC CAG AGA GAG GAT TTT GAG AAG AAG  
1344

Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys  
435                      440                      445

TAC TCC CGG AAG GTG GAT CCC CGC TTC GGA GCC TAC GTT GCC TGT GCC  
1392

Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala  
450                      455                      460

CTG TTG GTC TTC TGC TTC ATC TGC TTC ATC CAG CTT CTA ATT TTC CCA 1440  
Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro  
465                      470                      475                      480

CAC TCC ACC CTG ATG CTT GGG ATT TAT GCC AGC ATC TTC CTG CTG CTG  
1488

His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu  
485                      490                      495

CTA ATC ACC GTG CTG ATC TGT GCT GTG TAC TCC TGT GGT TCT CTG TTC 1536  
Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe  
500                      505                      510

CCT AAG GCC CTG CAA CGT CTG TCC CGC AGC ATT GTC CGC TCA CGG GCA  
1584

Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala  
515                      520                      525

CAT AGC ACC GCA GTT GGC ATC TTT TCC GTC CTG CTT GTG TTT ACT TCT 1632  
His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser  
530                      535                      540

GCC ATT GCC AAC ATG TTC ACC TGT AAC CAC ACC CCC ATA CGG AGC TGT  
1680

Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys  
545                      550                      555                      560

GCA GCC CGG ATG CTG AAT TTA ACA CCT GCT GAC ATC ACT GCC TGC CAC  
1728

Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His  
565 570 575

CTG CAG CAG CTC AAT TAC TCT CTG GGC CTG GAT GCT CCC CTG TGT GAG  
1776

Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu  
580 585 590

GGC ACC ATG CCC ACC TGC AGC TTT CCT GAG GTG TTC  
Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Phe  
595 600

1812

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val Gly Gly Ala  
1 5 10 15  
Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val  
20 25 30  
Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala  
35 40 45  
Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala  
50 55 60  
Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala  
65 70 75 80  
Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His  
85 90 95  
Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser  
100 105 110  
Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu  
115 120 125  
Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys



130            135            140  
 Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile  
 145            150            155            160  
 Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe  
           165            170            175  
 Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu  
           180            185            190  
 Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys  
           195            200            205  
 Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu  
           210            215            220  
 Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val  
 225            230            235            240  
 Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn  
           245            250            255  
 Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val  
           260            265            270  
 Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr  
           275            280            285  
 Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile  
           290            295            300  
 Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro  
 305            310            315            320  
 Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu  
           325            330            335  
 Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly  
           340            345            350  
 Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu  
           355            360            365  
 Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser  
           370            375            380  
 Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg  
 385            390            395            400  
 Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu  
           405            410            415  
 Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His  
           420            425            430  
 Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys  
           435            440            445  
 Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala  
           450            455            460  
 Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro  
 465            470            475            480  
 His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu  
           485            490            495

Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe  
 500 505 510  
 Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala  
 515 520 525  
 His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser  
 530 535 540  
 Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys  
 545 550 555 560  
 Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His  
 565 570 575  
 Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu  
 580 585 590  
 Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Phe  
 595 600

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...3501
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TCA TGG TTT AGT GGC CTC CTG GTC CCT AAA GTG GAT GAA CGG AAA  
48

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys  
1 5 10 15

ACA GCC TGG GGT GAA CGC AAT GGG CAG AAG CGT TCG CGG CGC CGT GGC  
96

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly  
20 25 30

ACT CGG GCA GGT GGC TTC TGC ACG CCC CGC TAT ATG AGC TGC CTC CGG  
144

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg  
35 40 45

GAT GCA GAG CCA CCC AGC CCC ACC CCT GCG GGC CCC CCT CGG TGC CCC  
192

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro  
50 55 60

TGG CAG GAT GAC GCC TTC ATC CGG AGG GGC GGC CCA GGC AAG GGC AAG  
240

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys  
65 70 75 80

GAG CTG GGG CTG CGG GCA GTG GCC CTG GGC TTC GAG GAT ACC GAG GTG  
288

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val  
85 90 95

ACA ACG ACA GCG GGC GGG ACG GCT GAG GTG GCG CCC GAC GCG GTG CCC  
336

Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro  
100 105 110

AGG AGT GGG CGA TCC TGC TGG CGC CGT TTG GTG CAG GTG TTC CAG TCG  
384

Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser  
115 120 125

AAG CAG TTC CGT TCG GCC AAG CTG GAG CGC CTG TAC CAG CGG TAC TTT  
432

Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe  
130 135 140

TTC CAG ATG AAC CAG AGC AGC CTG ACG CTG CTG GTG GCG GTG CTG GTG  
480

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Val Ala Val Leu Val  
145 150 155 160

CTG CTC ACA GCG GTG CTG CTG GCT TTC CAA GCC GCA CCC GCC CGC CCT  
528

Leu Leu Thr Ala Val Leu Leu Ala Phe Gln Ala Ala Pro Ala Arg Pro  
165 170 175

CAG CCT GCC TAT GTG GCA CTG TTG GCC TGT GCC GCC GCC CTG TTC GTG  
576

Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val  
180 185 190

GGG CTC ATG GTG GTG TGT AAC CGG CAT AGC TTC CGC CAG GAC TCC ATG  
624

Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met  
195 200 205

TGG GTG GTG AGT AAC GTG GTG CTG GGC ATC CTG GCG GCA GTG CAG GTC  
672

Trp Val Val Ser Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val  
210 215 220

GGG GGC GCT TTC GCA GCA GAC CCG CGC AGC CCC TCT GCG GGC CTC TGG  
720

Gly Gly Ala Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp  
225 230 235 240

TGC CCT GTG TTC TTT GTA TAC ATC GCA TAC ACG CTC CTC CCC ATC CGC 768  
Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg  
245 250 255

ATG CGG GCT GCC GTC CTC AGC GGC CTG GGC CTC TCC ACC TTG CAT TTG  
816

Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu  
260 265 270

ATC TTG GCC TGG CAA CTT AAC CGT GGT GAT GCC TTC CTC TGG AAG CAG  
864

Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln  
275 280 285

CTC GGT GCC AAT GTG CTG CTG TTC CTC TGC ACC AAC GTC ATT AGC ATC 912  
Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile  
290 295 300

TGC ACA CAC TAT CCA GCA GAG GTG TCT CAG CGC CAG GCC TTT CAG GAG  
960

Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu  
305 310 315 320

ACC CGC AGT TAC ATC CAG GCC CGG CTC CAC CTG CAG CAT GAG AAT CGG  
1008

Thr Arg Ser Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg  
325 330 335

CAG CAG GAG CGG CTG CTG CTG TCG GTA TTG CCC CAG CAC GTT GCC ATG  
1056

Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met  
340 345 350

GAG ATG AAA GAA GAC ATC AAC ACA AAA AAA GAA GAC ATG TTC CAC AAG  
1104

Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys  
355 360 365

ATC TAC ATA CAG AAG CAT GAC AAT GTC AGC ATC CTG TTT GCA GAC ATT  
1152

Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile  
370 375 380

GAG GGC TTC ACC AGC CTG GCA TCC CAG TGC ACT GCG CAG GAG CTG GTC  
1200

Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val  
385 390 395 400

ATG ACC CTG AAT GAG CTC TTT GCC CGG TTT GAC AAG CTG GCT GCG GAG  
1248

Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu  
405 410 415

AAT CAC TGC CTG AGG ATC AAG ATC TTG GGG GAC TGT TAC TAC TGT GTG  
1296

Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val  
420 425 430

TCA GGG CTG CCG GAG GCC CGG GCC GAC CAT GCC CAC TGC TGT GTG GAG  
1344

Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu  
435 440 445

ATG GGG GTA GAC ATG ATT GAG GCC ATC TCG CTG GTA CGT GAG GTG ACA  
1392

Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr  
450 455 460

GGT GTG AAT GTG AAC ATG CGC GTG GGC ATC CAC AGC GGG CGC GTG CAC  
1440

Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His  
465 470 475 480

TGC GGC GTC CTT GGC TTG CGG AAA TGG CAG TTC GAT GTG TGG TCC AAT  
1488

Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn  
485 490 495

GAT GTG ACC CTG GCC AAC CAC ATG GAA GCA GGA AGC CGG GCT GGC CGC  
1536

Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg  
500 505 510

ATC CAC ATC ACT CGG GCA ACA CTG CAG TAC CTG AAC GGG GAC TAC GAA  
1584

Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu  
515 520 525

GTG GAG CCA GGC CGT GGT GGC AAG CGC AAC GCG TAC CTC AAG GAG CAG  
1632

Val Glu Pro Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln  
530 535 540

CAC ATT GAG ACT TTC CTC ATC CTG GGC GCC AGC CAG AAA CGG AAA GAG  
1680

His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu  
545 550 555 560

GAG AAA GGC ATG CTG GCC AAG CTG CAG CGG ACT CGG GCC AAC TCC ATG  
1728

Glu Lys Gly Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met  
565 570 575

GAA GGG CTG ATG CCG CGA TGG GTT CCT GAT CGT GCC TTC TCC CGG ACC  
1776

Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr  
580 585 590

AAG GAC TCC AAG GCC TTC CGC CAG ATG GGC ATT GAT GAT TCC AGC AAA  
1824

Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys  
595 600 605

GAC AAC CGG GGC ACC CAA GAT GCC CTG AAC CCT GAG GAT GAG GTG GAT  
1872

Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp  
610 615 620

GAG TTC CTG AGC CGT GCC ATC GAT GCC CGC AGC ATT GAT CAG CTG CGG  
1920

Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg  
625                      630                      635                      640

AAG GAC CAT GTG CGC CGG TTT TTG CTC ACC TTC CAG AGA GAG GAT TTT  
1968

Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe  
645                      650                      655

GAG AAG AAG TAC TCC CGG AAG GTG GAT CCC CGC TTC GGA GCC TAC GTT  
2016

Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val  
660                      665                      670

GCC TGT GCC CTG TTG GTC TTC TGC TTC ATC TGC TTC ATC CAG CTT CTA    2064  
Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu

675                      680                      685

ATT TTC CCA CAC TCC ACC CTG ATG CTT GGG ATT TAT GCC AGC ATC TTC    2112  
Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe

690                      695                      700

CTG CTG CTG CTA ATC ACC GTG CTG ATC TGT GCT GTG TAC TCC TGT GGT  
2160

Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly  
705                      710                      715                      720

TCT CTG TTC CCT AAG GCC CTG CAA CGT CTG TCC CGC AGC ATT GTC CGC  
2208

Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg  
725                      730                      735

TCA CGG GCA CAT AGC ACC GCA GTT GGC ATC TTT TCC GTC CTG CTT GTG  
2256

Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val  
740                      745                      750

TTT ACT TCT GCC ATT GCC AAC ATG TTC ACC TGT AAC CAC ACC CCC ATA  
2304

Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile  
755                      760                      765

CGG AGC TGT GCA GCC CGG ATG CTG AAT TTA ACA CCT GCT GAC ATC ACT  
2352

Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr  
770 775 780

GCC TGC CAC CTG CAG CAG CTC AAT TAC TCT CTG GGC CTG GAT GCT CCC  
2400

Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro  
785 790 795 800

CTG TGT GAG GGC ACC ATG CCC ACC TGC AGC TTT CCT GAG GTG TCC ATC  
2448

Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Ser Ile  
805 810 815

GGG AAC ATG CTG CTG AGT CTC TTG GCC AGC TCT GTC TTC CTG CAC ATC  
2496

Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile  
820 825 830

AGC AGC ATC GGG AAG TTG GCC ATG ATC TTT GTC TTG GGG CTC ATC TAT  
2544

Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr  
835 840 845

TTG GTG CTG CTT CTG CTG GGT CCC CCA GCC GCC ATC TTT GAC AAC TAT  
2592

Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Ala Ile Phe Asp Asn Tyr  
850 855 860

GAC CTA CTG CTT GGC GTC CAT GGC TTG GCT TCT TCC AAT GAG ACC TTT  
2640

Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe  
865 870 875 880

GAT GGG CTG GAC TGT CCA GCT GCA GGG AGG GTG GCC CTC AAA TAT ATG  
2688

Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met  
885 890 895

ACC CCT GTG ATT CTG CTG GTG TTT GCG CTG GCG CTG TAT CTG CAT GCT  
2736

Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala  
900 905 910

CAG CAG GTG GAA TCG ACT GCC CGC CTA AAC TTC CTC TGG AAA CTA CAG  
2784



Gln Gln Val Glu Ser Thr Ala Arg Leu Asn Phe Leu Trp Lys Leu Gln  
 915 920 925

GCA ACA GGG GAA AAA GAG GAG ATG GAG GAG CTA CAG GCA TAC AAC CGG  
 2832

Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg  
 930 935 940

AGG CTG CTG CAT AAC ATT CTG CCC AAG GAC GTG GCG GCC CAC TTC CTG  
 2880

Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu  
 945 950 955 960

GCC CGG GAG CGC CGC AAT GAT GAA CTC TAC TAT CAG TCG TGT GAG TGT  
 2928

Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys  
 965 970 975

GTG GCT GTT ATG TTT GCC TCC ATT GCC AAC TTC TCT GAG TTC TAT GTG 2976  
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val  
 980 985 990

GAG CTG GAG GCA AAC AAT GAG GGT GCC GAG TGC CTG CGG CTG CTC AAC  
 3024

Glu Leu Glu Ala Asn Asn Glu Gly Ala Glu Cys Leu Arg Leu Leu Asn  
 995 1000 1005

GAG ATC ATC GCT GAC TTT GAT GAG ATT ATC AGC GAG GAG CGG TTC CGG  
 3072

Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg  
 1010 1015 1020

CAG CTG GAA AAG ATC AAG ACG ATT GGT AGC ACC TAC ATG GCT GCC TCA  
 3120

Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser  
 1025 1030 1035 1040

GGG CTG AAC GCC AGC ACC TAC GAT CAG GTG GGC CGC TCC CAC ATC ACT  
 3168

Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr  
 1045 1050 1055

GCC CTG GCT GAC TAC GCC ATG CGG CTC ATG GAG CAG ATG AAG CAC ATC  
 3216

Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile

pa-550552

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys  
 1           5           10           15  
 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly  
           20           25           30  
 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg  
           35           40           45  
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro  
           50           55           60  
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys  
 65           70           75           80  
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val  
           85           90           95  
 Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro  
           100           105           110  
 Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser  
           115           120           125  
 Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe  
           130           135           140  
 Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Val Ala Val Leu Val  
 145           150           155           160  
 Leu Leu Thr Ala Val Leu Leu Ala Phe Gln Ala Ala Pro Ala Arg Pro  
           165           170           175  
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val  
           180           185           190  
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met  
           195           200           205  
 Trp Val Val Ser Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val  
           210           215           220  
 Gly Gly Ala Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp  
 225           230           235           240  
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg  
           245           250           255  
 Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu  
           260           265           270  
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln  
           275           280           285  
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile  
           290           295           300  
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu  
 305           310           315           320  
 Thr Arg Ser Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg  
           325           330           335  
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met

340                    345                    350  
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys  
 355                    360                    365  
 Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile  
 370                    375                    380  
 Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val  
 385                    390                    395                    400  
 Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu  
 405                    410                    415  
 Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val  
 420                    425                    430  
 Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu  
 435                    440                    445  
 Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr  
 450                    455                    460  
 Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His  
 465                    470                    475                    480  
 Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn  
 485                    490                    495  
 Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg  
 500                    505                    510  
 Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu  
 515                    520                    525  
 Val Glu Pro Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln  
 530                    535                    540  
 His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu  
 545                    550                    555                    560  
 Glu Lys Gly Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met  
 565                    570                    575  
 Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr  
 580                    585                    590  
 Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys  
 595                    600                    605  
 Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp  
 610                    615                    620  
 Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg  
 625                    630                    635                    640  
 Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe  
 645                    650                    655  
 Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val  
 660                    665                    670  
 Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu  
 675                    680                    685  
 Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe  
 690                    695                    700

Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly  
 705            710            715            720  
 Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg  
               725            730            735  
 Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val  
               740            745            750  
 Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile  
               755            760            765  
 Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr  
               770            775            780  
 Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro  
 785            790            795            800  
 Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Ser Ile  
               805            810            815  
 Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile  
               820            825            830  
 Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr  
               835            840            845  
 Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Ala Ile Phe Asp Asn Tyr  
               850            855            860  
 Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe  
 865            870            875            880  
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met  
               885            890            895  
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala  
               900            905            910  
 Gln Gln Val Glu Ser Thr Ala Arg Leu Asn Phe Leu Trp Lys Leu Gln  
               915            920            925  
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg  
               930            935            940  
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu  
 945            950            955            960  
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys  
               965            970            975  
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val  
               980            985            990  
 Glu Leu Glu Ala Asn Asn Glu Gly Ala Glu Cys Leu Arg Leu Leu Asn  
               995            1000            1005  
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg  
               1010            1015            1020  
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser  
 025            1030            1035            1040  
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr  
               1045            1050            1055  
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile

1060                      1065                      1070  
 Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met  
 1075                      1080                      1085  
 Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp  
 1090                      1095                      1100  
 Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly  
 105                      1110                      1115                      1120  
 Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala  
 1125                      1130                      1135  
 Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly  
 1140                      1145                      1150  
 Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser  
 1155                      1160                      1165

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACGTAGAATT CGGRGAYTGT TAYTACTG

28

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACGTTAAGCT TCCASACRTC RAAYTGCCA

29

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA  
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

UUAUUUAWW

9

<210> 10  
 <211> 3552  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(3507)

<400> SEQ ID NO:10

atg tca tgg ttg agt ggc ctc ctg gtc cct aaa gtg gat gaa cgg aaa 48  
 Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys  
 1 5 10 15

aca gcc tgg ggt gaa cgc aat ggg cag aag cgt tgc cgg cgc cgt ggc 96  
 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly  
 20 25 30

act cgg gca ggt ggc ttc tgc acg ccc cgc tat atg agc tgc ctc cgg 144  
 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg  
 35 40 45

gat gca gag cca ccc agc ccc acc cct gcg ggc ccc cct cgg tgc ccc 192  
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro  
 50 55 60

tgg cag gat gac gcc ttc atc cgg agg ggc ggc cca ggc aag ggc aag 240  
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys  
 65 70 75 80

gag ctg ggg ctg cgg gca gtg gcc ctg ggc ttc gag gat acc gag gtg 288  
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85                      90                      95

aca acg aca gcg ggc ggg acg gct gag gtg gcg ccc gac gcg gtg ccc 336  
Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro  
100                      105                      110

agg agt ggg cga tcc tgc tgg cgc cgt ctg gtg cag gtg ttc cag tcg 384  
Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser  
115                      120                      125

aag cag ttc cgt tcg gcc aag ctg gag cgc ctg tac cag cgg tac ttc 432  
Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe  
130                      135                      140

ttc cag atg aac cag agc agc ctg acg ctg ctg atg gcg gtg ctg gtg 480  
Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val  
145                      150                      155                      160

ctg ctc aca gcg gtg ctg ctg gct ttc cac gcc gca ccc gcc cgc cct 528  
Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro  
165                      170                      175

cag cct gcc tat gtg gca ctg ttg gcc tgt gcc gcc gcc ctg ttc gtg 576  
Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val  
180                      185                      190

ggg ctc atg gtg gtg tgt aac cgg cat agc ttc cgc cag gac tcc atg 624  
Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met  
195                      200                      205

tgg gtg gtg agt tac gtg gtg ctg ggc atc ctg gcg gca gtg cag gtc 672  
Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val  
210                      215                      220

ggg ggc gct ctc gca gca gac ccg cgc agc ccc tct gcg ggc ctc tgg 720  
Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp  
225                      230                      235                      240

tgc cct gtg ttc ttt gtc tac atc gcc tac acg ctc ctc ccc atc cgc 768  
Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg  
245                      250                      255

atg cgg gct gcc gtc ctc agc ggc ctg ggc ctc tcc acc ttg cat ttg 816  
Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu  
260                      265                      270



atc ttg gcc tgg caa ctt aac cgt ggt gat gcc ttc ctc tgg aag cag 864  
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln  
 275 280 285

ctc ggt gcc aat gtg ctg ctg ttc ctc tgc acc aac gtc att ggc atc 912  
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile  
 290 295 300

tgc aca cac tat cca gca gag gtg tct cag cgc cag gcc ttt cag gag 960  
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu  
 305 310 315 320

acc cgc ggt tac atc cag gcc cgg ctc cac ctg cag cat gag aat cgg 1008  
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg  
 325 330 335

cag cag gag cgg ctg ctg ctg tgc gta ttg ccc cag cac gtt gcc atg 1056  
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met  
 340 345 350

gag atg aaa gaa gac atc aac aca aaa aaa gaa gac atg atg ttc cac 1104  
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His  
 355 360 365

aag atc tac ata cag aag cat gac aat gtc agc atc ctg ttt gca gac 1152  
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp  
 370 375 380

att gag ggc ttc acc agc ctg gca tcc cag tgc act gcg cag gag ctg 1200  
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu  
 385 390 395 400

gtc atg acc ctg aat gag ctc ttt gcc cgg ttt gac aag ctg gct gcg 1248  
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala  
 405 410 415

gag aat cac tgc ctg agg atc aag atc ttg ggg gac tgt tac tac tgt 1296  
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys  
 420 425 430

gtg tca ggg ctg ccg gag gcc cgg gcc gac cat gcc cac tgc tgt gtg 1344  
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val  
 435 440 445

009997-04635260

gag atg ggg gta gac atg att gag gcc atc tcg ctg gta cgt gag gtg 1392  
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val  
 450 455 460

aca ggt gtg aat gtg aac atg cgc gtg ggc atc cac agc ggg cgc gtg 1440  
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val  
 465 470 475 480

cac tgc ggc gtc ctt ggc ttg cgg aaa tgg cag ttc gat gtg tgg tcc 1488  
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser  
 485 490 495

aat gat gtg acc ctg gcc aac cac atg gag gca gga ggc cgg gct ggc 1536  
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Arg Ala Gly  
 500 505 510

cgc atc cac atc act cgg gca aca ctg cag tac ctg aac ggg gac tac 1584  
 Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr  
 515 520 525

gag gtg gag cca ggc cgt ggt ggc gag cgc aac gcg tac ctc aag gag 1632  
 Glu Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu  
 530 535 540

cag cac att gag act ttc ctc atc ctg ggc gcc agc cag aaa cgg aaa 1680  
 Gln His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys  
 545 550 555 560

gag gag aag gcc atg ctg gcc aag ctg cag cgg act cgg gcc aac tcc 1728  
 Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser  
 565 570 575

atg gaa ggg ctg atg ccg cgc tgg gtt cct gat cgt gcc ttc tcc cgg 1776  
 Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg  
 580 585 590

acc aag gac tcc aag gcc ttc cgc cag atg ggc att gat gat tcc agc 1824  
 Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser  
 595 600 605

aaa gac aac cgg ggc acc caa gat gcc ctg aac cct gag gat gag gtg 1872  
 Lys Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val  
 610 615 620

gat gag ttc ctg agc cgt gcc atc gat gcc cgc agc att gat cag ctg 1920

Asp Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu  
625                    630                    635                    640

cgg aag gac cat gtg cgc cgg ttt ctg ctc acc ttc cag aga gag gat 1968  
Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp  
645                    650                    655

ctt gag aag aag tac tcc cgg aag gtg gat ccc cgc ttc gga gcc tac 2016  
Leu Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr  
660                    665                    670

gtt gcc tgt gcc ctg ttg gtc ttc tgc ttc atc tgc ttc atc cag ctt 2064  
Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu  
675                    680                    685

ctc atc ttc cca cac tcc acc ctg atg ctt ggg atc tat gcc agc atc 2112  
Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile  
690                    695                    700

ttc ctg ctg ctg cta atc acc gtg ctg atc tgt gct gtg tac tcc tgt 2160  
Phe Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys  
705                    710                    715                    720

ggt tct ctg ttc cct aag gcc ctg caa cgt ctg tcc cgc agc att gtc 2208  
Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val  
725                    730                    735

cgc tca cgg gca cat agc acc gca gtt ggc atc ttt tcc gtc ctg ctt 2256  
Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu  
740                    745                    750

gtg ttt act tct gcc att gcc aac atg ttc acc tgt aac cac acc ccc 2304  
Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro  
755                    760                    765

ata cgg agc tgt gca gcc cgg atg ctg aat tta aca cct gct gac atc 2352  
Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile  
770                    775                    780

act gcc tgc cac ctg cag cag ctc aat tac tct ctg ggc ctg gat gct 2400  
Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala  
785                    790                    795                    800

ccc ctg tgt gag ggc acc atg ccc acc tgc agc ttt cct gag tac ttc 2448  
Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe

805                      810                      815

atc ggg aac atg ctg ctg agt ctc ttg gcc agc tct gtc ttc ctg cac 2496  
Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His  
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atc agc agc atc ggg aag ttg gcc atg atc ttt gtc ttg ggg ctc atc 2544  
Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile  
835                      840                      845

tat ttg gtg ctg ctt ctg ctg ggt ccc cca gcc acc atc ttt gac aac 2592  
Tyr Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn  
850                      855                      860

tat gac cta ctg ctt ggc gtc cat ggc ttg gct tct tcc aat gag acc 2640  
Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr  
865                      870                      875                      880

ttl gat ggg ctg gac tgt cca gct gca ggg agg gtg gcc ctc aaa tat 2688  
Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr  
885                      890                      895

atg acc cct gtg att ctg ctg gtg ttt gcg ctg gcg ctg tat ctg cat 2736  
Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His  
900                      905                      910

gct cag cag gtg gag tcg act gcc cgc cta gac ttc ctc tgg aaa cta 2784  
Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu  
915                      920                      925

cag gca aca ggg gag aag gag gag atg gag gag cta cag gca tac aac 2832  
Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn  
930                      935                      940

cgg agg ctg ctg cat aac att ctg ccc aag gac gtg gcg gcc cac ttc 2880  
Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe  
945                      950                      955                      960

ctg gcc cgg gag cgc cgc aat gat gaa ctc tac tat cag tcg tgt gag 2928  
Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu  
965                      970                      975

tgt gtg gct gtt atg ttt gcc tcc att gcc aac ttc tct gag ttc tat 2976  
Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr  
980                      985                      990

gtg gag ctg gag gca aac aat gag ggt gtc gag tgc ctg cgg ctg ctc 3024  
Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu  
995 1000 1005

aac gag atc atc gct gac ttt gat gag att atc agc gag gag cgg ttc 3072  
Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe  
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cgg cag ctg gaa aag atc aag acg att ggt agc acc tac atg gct gcc 3120  
Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala  
1025 1030 1035 1040

tca ggg ctg aac gcc agc acc tac gat cag gtg ggc cgc tcc cac atc 3168  
Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile  
1045 1050 1055

act gcc ctg gct gac tac gcc atg cgg ctc atg gag cag atg aag cac 3216  
Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His  
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atc aat gag cac tcc ttc aac aat ttc cag atg aag att ggg ctg aac 3264  
Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn  
1075 1080 1085

atg ggc cca gtc gtg gca ggt gtc atc ggg gct cgg aag cca cag tat 3312  
Met Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr  
1090 1095 1100

gac atc tgg ggg aac aca gtg aat gtc tct agt cgt atg gac agc acg 3360  
Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr  
1105 1110 1115 1120

ggg gtc ccc gac cga atc cag gtg acc acg gac ctg tac cag gtt cta 3408  
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1125 1130 1135

gct gcc aag ggc tac cag ctg gag tgt cga ggg gtg gtc aag gtg aag 3456  
Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys  
1140 1145 1150

ggc aag ggg gag atg acc acc tac ttc ctc aat ggg ggc ccc agc agt 3504  
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taa cagggccccag ccacaaattc agctgaaggg accaaggtgg gcact 3552

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35 40 45

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro

50 55 60

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys

65 70 75 80

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85 90 95

Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro

100 105 110

Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser

115 120 125

Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe

130 135 140

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val

145 150 155 160

Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro

165 170 175

Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val

180 185 190

Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met

195 200 205

Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val

210 215 220

Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp

225 230 235 240

Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg

245 250 255

Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu

260 265 270

Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln

275            280            285  
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile  
 290            295            300  
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu  
 305            310            315            320  
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg  
 325            330            335  
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met  
 340            345            350  
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His  
 355            360            365  
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp  
 370            375            380  
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu  
 385            390            395            400  
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala  
 405            410            415  
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys  
 420            425            430  
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val  
 435            440            445  
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val  
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 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val  
 465            470            475            480  
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser  
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 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Arg Ala Gly  
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 Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr  
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 Glu Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu  
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 Gln His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys  
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 Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser  
 565            570            575  
 Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg  
 580            585            590  
 Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser  
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 Lys Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val  
 610            615            620  
 Asp Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu  
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Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp  
 645 650 655  
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 Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu  
 675 680 685  
 Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile  
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 Phe Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys  
 705 710 715 720  
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 Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu  
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 Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro  
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 Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe  
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 Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His  
 820 825 830  
 Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile  
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 Tyr Leu Val Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn  
 850 855 860  
 Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr  
 865 870 875 880  
 Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr  
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 Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His  
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 Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu  
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 Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn  
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 Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe  
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 Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu  
 965 970 975  
 Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr  
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 Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu



995            1000            1005  
 Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe  
 1010            1015            1020  
 Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala  
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 Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile  
 1045            1050            1055  
 Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His  
 1060            1065            1070  
 Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn  
 1075            1080            1085  
 Met Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr  
 1090            1095            1100  
 Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr  
 1105            1110            1115            1120  
 Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu  
 1125            1130            1135  
 Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys  
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 Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser  
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aaa gtg gat gaa cgg aaa aca gcc tgg ggt gaa cgc aat ggg cag aag 99  
 Lys Val Asp Glu Arg Lys Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys  
                   15            20            25

cgt tcg cgg cgc cgt ggc act cgg gca ggt ggc ttc tgc acg ccc cgc 147

Arg Ser Arg Arg Arg Gly Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg  
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tat atg agc tgc ctc cgg gat gca gag cca ccc agc ccc acc cct gcg 195  
 Tyr Met Ser Cys Leu Arg Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala  
 45 50 55

ggc ccc cct cgg tgc ccc tgg cag gat gac gcc ttc atc cgg agg ggc 243  
 Gly Pro Pro Arg Cys Pro Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly  
 60 65 70

ggc cca ggc aag ggc aag gag ctg ggg ctg cgg gca gtg gcc ctg ggc 291  
 Gly Pro Gly Lys Gly Lys Glu Leu Gly Leu Arg Ala Val Ala Leu Gly  
 75 80 85 90

ttc gag gat acc gag gtg aca acg aca gcg ggc ggg acg gct gag gtg 339  
 Phe Glu Asp Thr Glu Val Thr Thr Thr Ala Gly Gly Thr Ala Glu Val  
 95 100 105

gcg ccc gac gcg gtg ccc agg agt ggg cga tcc tgc tgg cgc cgt ctg 387  
 Ala Pro Asp Ala Val Pro Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu  
 110 115 120

gtg cag gtg ttc cag tgc aag cag ttc cgt tgc gcc aag ctg gag cgc 435  
 Val Gln Val Phe Gln Ser Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg  
 125 130 135

ctg tac cag cgg tac ttc ttc cag atg aac cag agc agc ctg acg ctg 483  
 Leu Tyr Gln Arg Tyr Phe Phe Gln Met Asn Gln Ser Ser Leu Thr Leu  
 140 145 150

ctg atg gcg gtg ctg gtg ctg ctc aca gcg gtg ctg ctg gct ttc cac 531  
 Leu Met Ala Val Leu Val Leu Leu Thr Ala Val Leu Leu Ala Phe His  
 155 160 165 170

gcc gca ccc gcc cgc cct cag cct gcc tat gtg gca ctg ttg gcc tgt 579  
 Ala Ala Pro Ala Arg Pro Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys  
 175 180 185

gcc gcc gcc ctg ttc gtg ggg ctc atg gtg gtg tgt aac cgg cat agc 627  
 Ala Ala Ala Leu Phe Val Gly Leu Met Val Val Cys Asn Arg His Ser  
 190 195 200

ttc cgc cag gac tcc atg tgg gtg gtg agt tac gtg gtg ctg ggc atc 675  
 Phe Arg Gln Asp Ser Met Trp Val Val Ser Tyr Val Val Leu Gly Ile

205                      210                      215

ctg gcg gca gtg cag gtc ggg ggc gct ctc gca gca gac ccg cgc agc 723  
Leu Ala Ala Val Gln Val Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser  
220                      225                      230

ccc tct gcg ggc ctc tgg tgc cct gtg ttc ttt gtc tac atc gcc tac 771  
Pro Ser Ala Gly Leu Trp Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr  
235                      240                      245                      250

acg ctc ctc ccc atc cgc atg cgg gct gcc gtc ctc agc ggc ctg ggc 819  
Thr Leu Leu Pro Ile Arg Met Arg Ala Ala Val Leu Ser Gly Leu Gly  
255                      260                      265

ctc tcc acc ttg cat ttg atc ttg gcc tgg caa ctt aac cgt ggt gat 867  
Leu Ser Thr Leu His Leu Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp  
270                      275                      280

gcc ttc ctc tgg aag cag ctc ggt gcc aat gtg ctg ctg ttc ctc tgc 915  
Ala Phe Leu Trp Lys Gln Leu Gly Ala Asn Val Leu Leu Phe Leu Cys  
285                      290                      295

acc aac gtc att ggc atc tgc aca cac tat cca gca gag gtg tct cag 963  
Thr Asn Val Ile Gly Ile Cys Thr His Tyr Pro Ala Glu Val Ser Gln  
300                      305                      310

cgc cag gcc ttt cag gag acc cgc ggt tac atc cag gcc cgg ctc cac 1011  
Arg Gln Ala Phe Gln Glu Thr Arg Gly Tyr Ile Gln Ala Arg Leu His  
315                      320                      325                      330

ctg cag cat gag aat cgg cag cag gag cgg ctg ctg ctg tgc gta ttg 1059  
Leu Gln His Glu Asn Arg Gln Gln Glu Arg Leu Leu Leu Ser Val Leu  
335                      340                      345

ccc cag cac gtt gcc atg gag atg aaa gaa gac atc aac aca aaa aaa 1107  
Pro Gln His Val Ala Met Glu Met Lys Glu Asp Ile Asn Thr Lys Lys  
350                      355                      360

gaa gac atg atg ttc cac aag atc tac ata cag aag cat gac aat gtc 1155  
Glu Asp Met Met Phe His Lys Ile Tyr Ile Gln Lys His Asp Asn Val  
365                      370                      375

agc atc ctg ttt gca gac att gag ggc ttc acc agc ctg gca tcc cag 1203  
Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln  
380                      385                      390

tgc act gcg cag gag ctg gtc atg acc ttg aat gag ctc ttt gcc cgg 1251  
 Cys Thr Ala Gln Glu Leu Val Met Thr Leu Asn Glu Leu Phe Ala Arg  
 395 400 405 410

ttt gac aag ctg gct gcg gag aat cac tgt ctg agg atc aag atc tta 1299  
 Phe Asp Lys Leu Ala Ala Glu Asn His Cys Leu Arg Ile Lys Ile Leu  
 415 420 425

gga gac tgt tac tac tgc gtg tca ggg ctg ccc gag gcc cgg gca gat 1347  
 Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu Pro Glu Ala Arg Ala Asp  
 430 435 440

cac gcc cac tgc tgt gtg gag atg ggg gta gac atg atc gaa gcc atc 1395  
 His Ala His Cys Cys Val Glu Met Gly Val Asp Met Ile Glu Ala Ile  
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tcg ctg gtg cgt gag gta aca ggt gtg aac gtg aac atg cgt gtg ggc 1443  
 Ser Leu Val Arg Glu Val Thr Gly Val Asn Val Asn Met Arg Val Gly  
 460 465 470

atc cac agc gga cgt gtg cat tgc ggc gtc ctt ggc cta cgg aaa tgg 1491  
 Ile His Ser Gly Arg Val His Cys Gly Val Leu Gly Leu Arg Lys Trp  
 475 480 485 490

cag ttt gat gtc tgg tca aac gat gtg acc ctg gct aac cac atg gag 1539  
 Gln Phe Asp Val Trp Ser Asn Asp Val Thr Leu Ala Asn His Met Glu  
 495 500 505

gcc ggg ggc ggc cgg cgc atc cac atc act cgg gct aca ctg cag tac 1587  
 Ala Gly Gly Gly Arg Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr  
 510 515 520

ttg aac ggg gac tat gag gtg gag cca ggc cgt ggt ggt gaa cgc aat 1635  
 Leu Asn Gly Asp Tyr Glu Val Glu Pro Gly Arg Gly Gly Glu Arg Asn  
 525 530 535

gcg tac ctc aag gag cag tgc att gag acc ttc ctc ata ctt ggc gcc 1683  
 Ala Tyr Leu Lys Glu Gln Cys Ile Glu Thr Phe Leu Ile Leu Gly Ala  
 540 545 550

agc caa aaa cgg aaa gag gag aaa gcc atg ctg gcc aag ctt cag cgg 1731  
 Ser Gln Lys Arg Lys Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg  
 555 560 565 570

aca cgg gcc aac tcc atg gaa gga ctg atg ccc cgc tgg gtt cct gac 1779  
 Thr Arg Ala Asn Ser Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp  
           575              580              585

cgt gcc ttc tcc cgg acc aag gac tct aag gca ttc cgc cag atg ggc 1827  
 Arg Ala Phe Ser Arg Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly  
           590              595              600

att gat gat tct agc aaa gac aac cgg ggt gcc caa gat gct ctg aac 1875  
 Ile Asp Asp Ser Ser Lys Asp Asn Arg Gly Ala Gln Asp Ala Leu Asn  
           605              610              615

cct gaa gat gag gtg gat gag ttc ctg ggc cga gcc atc gat gcc cgc 1923  
 Pro Glu Asp Glu Val Asp Glu Phe Leu Gly Arg Ala Ile Asp Ala Arg  
           620              625              630

agc att gat cag ctg cgg aag gac cat gtg cgc cgg ttt ctg ctc acc 1971  
 Ser Ile Asp Gln Leu Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr  
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ttc cag aga gag gat ctt gag aag aag tac tcc cgg aag gtg gat ccc 2019  
 Phe Gln Arg Glu Asp Leu Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro  
           655              660              665

cgc ttc gga gcc tac gtt gcc tgt gcc ctg ttg gtc ttc tgc ttc atc 2067  
 Arg Phe Gly Ala Tyr Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile  
           670              675              680

tgc ttc atc cag ctt ctc atc ttc cca cac tcc acc ctg atg ctt ggg 2115  
 Cys Phe Ile Gln Leu Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly  
           685              690              695

atc tat gcc agc atc ttc ctg ctg ctg cta atc acc gtg ctg atc tgt 2163  
 Ile Tyr Ala Ser Ile Phe Leu Leu Leu Leu Ile Thr Val Leu Ile Cys  
           700              705              710

gct gtg tac tcc tgt ggt tct ctg ttc cct aag gcc ctg caa cgt ctg 2211  
 Ala Val Tyr Ser Cys Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu  
           715              720              725              730

tcc cgc agc att gtc cgc tca cgg gca cat agc acc gca gtt ggc atc 2259  
 Ser Arg Ser Ile Val Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile  
           735              740              745

ttt tcc gtc ctg ctt gtg ttt act tct gcc att gcc aac atg ttc acc 2307

Phe Ser Val Leu Leu Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr  
750 755 760

tgt aac cac acc ccc ata cgg agc tgt gca gcc cgg atg ctg aat tta 2355  
Cys Asn His Thr Pro Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu  
765 770 775

aca cct gct gac atc act gcc tgc cac ctg cag cag ctc aat tac tct 2403  
Thr Pro Ala Asp Ile Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser  
780 785 790

ctg gcc ctg gat gct ccc ctg tgt gag gcc acc atg ccc acc tgc agc 2451  
Leu Gly Leu Asp Ala Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser  
795 800 805 810

ttt cct gag tac ttc atc ggg aac atg ctg ctg agt ctc ttg gcc agc 2499  
Phe Pro Glu Tyr Phe Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser  
815 820 825

tct gtc ttc ctg cac atc agc agc atc ggg aag ttg gcc atg atc ttt 2547  
Ser Val Phe Leu His Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe  
830 835 840

gtc ttg ggg ctc atc tat ttg gtg ctg ctt ctg ctg ggt ccc cca gcc 2595  
Val Leu Gly Leu Ile Tyr Leu Val Leu Leu Leu Gly Pro Pro Ala  
845 850 855

acc atc ttt gac aac tat gac cta ctg ctt ggc gtc cat ggc ttg gct 2643  
Thr Ile Phe Asp Asn Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala  
860 865 870

tct tcc aat gag acc ttt gat ggg ctg gac tgt cca gct gca ggg agg 2691  
Ser Ser Asn Glu Thr Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg  
875 880 885 890

gtg gcc ctc aaa tat atg acc cct gtg att ctg ctg gtg ttt gcg ctg 2739  
Val Ala Leu Lys Tyr Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu  
895 900 905

gcg ctg tat ctg cat gct cag cag gtg gag tcg act gcc cgc cta gac 2787  
Ala Leu Tyr Leu His Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp  
910 915 920

ttc ctc tgg aaa cta cag gca aca ggg gag aag gag gag atg gag gag 2835  
Phe Leu Trp Lys Leu Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu

925                      930                      935

cta cag gca tac aac cgg agg ctg ctg cat aac att ctg ccc aag gac 2883  
Leu Gln Ala Tyr Asn Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp  
940                      945                      950

gtg gcg gcc cac ttc ctg gcc cgg gag cgc cgc aat gat gaa ctc tac 2931  
Val Ala Ala His Phe Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr  
955                      960                      965                      970

tat cag tcg tgt gag tgt gtg gct gtt atg ttt gcc tcc att gcc aac 2979  
Tyr Gln Ser Cys Glu Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn  
975                      980                      985

ttc tct gag ttc tat gtg gag ctg gag gca aac aat gag ggt gtc gag 3027  
Phe Ser Glu Phe Tyr Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu  
990                      995                      1000

tgc ctg cgg ctg ctc aac gag atc atc gct gac ttt gat gag att atc 3075  
Cys Leu Arg Leu Leu Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile  
1005                      1010                      1015

agc gag gag cgg ttc cgg cag ctg gaa aag atc aag acg att ggt agc 3123  
Ser Glu Glu Arg Phe Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser  
1020                      1025                      1030

acc tac atg gct gcc tca ggg ctg aac gcc agc acc tac gat cag gtg 3171  
Thr Tyr Met Ala Ala Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val  
1035                      1040                      1045                      1050

ggc cgc tcc cac atc act gcc ctg gct gac tac gcc atg cgg ctc atg 3219  
Gly Arg Ser His Ile Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met  
1055                      1060                      1065

gag cag atg aag cac atc aat gag cac tcc ttc aac aat ttc cag atg 3267  
Glu Gln Met Lys His Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met  
1070                      1075                      1080

aag att ggg ctg aac atg ggc cca gtc gtg gca ggt gtc atc ggg gct 3315  
Lys Ile Gly Leu Asn Met Gly Pro Val Val Ala Gly Val Ile Gly Ala  
1085                      1090                      1095

cgg aag cca cag tat gac atc tgg ggg aac aca gtg aat gtc tct agt 3363  
Arg Lys Pro Gln Tyr Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser  
1100                      1105                      1110

cgt atg gac agc acg ggg gtc ccc gac cga atc cag gtg acc acg gac 3411  
 Arg Met Asp Ser Thr Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp  
 1115 1120 1125 1130

ctg tac cag gtt cta gct gcc aag ggc tac cag ctg gag tgt cga ggg 3459  
 Leu Tyr Gln Val Leu Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly  
 1135 1140 1145

gtg gtc aag gtg aag ggc aag ggg gag atg acc acc tac ttc ctc aat 3507  
 Val Val Lys Val Lys Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn  
 1150 1155 1160

ggg ggc ccc agc agt taa cagggccag ccacaaattc agctgaaggg 3555  
 Gly Gly Pro Ser Ser  
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accaaggtgg gcactaaggg cgaattc 3582

<210> 13

<211> 1167

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified AC-VI

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 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly  
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 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg  
 35 40 45  
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro  
 50 55 60  
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys  
 65 70 75 80  
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val  
 85 90 95  
 Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro  
 100 105 110  
 Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser  
 115 120 125  
 Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe  
 130 135 140



Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val  
 145            150            155            160  
 Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro  
           165            170            175  
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val  
           180            185            190  
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met  
           195            200            205  
 Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val  
           210            215            220  
 Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp  
 225            230            235            240  
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg  
           245            250            255  
 Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu  
           260            265            270  
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln  
           275            280            285  
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile  
           290            295            300  
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu  
 305            310            315            320  
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg  
           325            330            335  
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met  
           340            345            350  
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His  
           355            360            365  
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp  
           370            375            380  
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu  
 385            390            395            400  
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala  
           405            410            415  
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys  
           420            425            430  
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val  
           435            440            445  
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val  
           450            455            460  
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val  
 465            470            475            480  
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser  
           485            490            495  
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Gly Arg Arg

500            505            510  
 Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu  
 515            520            525  
 Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu Gln  
 530            535            540  
 Cys Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu  
 545            550            555            560  
 Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met  
 565            570            575  
 Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr  
 580            585            590  
 Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys  
 595            600            605  
 Asp Asn Arg Gly Ala Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp  
 610            615            620  
 Glu Phe Leu Gly Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg  
 625            630            635            640  
 Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Leu  
 645            650            655  
 Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val  
 660            665            670  
 Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu  
 675            680            685  
 Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe  
 690            695            700  
 Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly  
 705            710            715            720  
 Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg  
 725            730            735  
 Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val  
 740            745            750  
 Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile  
 755            760            765  
 Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr  
 770            775            780  
 Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro  
 785            790            795            800  
 Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe Ile  
 805            810            815  
 Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile  
 820            825            830  
 Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr  
 835            840            845  
 Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn Tyr  
 850            855            860

Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe  
 865                870                875                880  
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met  
                  885                890                895  
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala  
                  900                905                910  
 Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu Gln  
                  915                920                925  
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg  
                  930                935                940  
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu  
 945                950                955                960  
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys  
                  965                970                975  
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val  
                  980                985                990  
 Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu Asn  
                  995                1000                1005  
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg  
                  1010                1015                1020  
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser  
 1025                1030                1035                1040  
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr  
                  1045                1050                1055  
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile  
                  1060                1065                1070  
 Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met  
                  1075                1080                1085  
 Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp  
                  1090                1095                1100  
 Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly  
 1105                1110                1115                1120  
 Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala  
                  1125                1130                1135  
 Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly  
                  1140                1145                1150  
 Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser  
                  1155                1160                1165